

## SEQUENCE LISTING

<110> Kosan Biosciences, Inc. Julien, Bryan <120> TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS BACTERIOPHAGE MX9 <130> 300622009940 <140> US 10/645,818 <141> 2003-08-20 <150> US 60/405,196 <151> 2002-08-21 <160> 20 <170> FastSEO for Windows Version 4.0 <210> 1 <211> 1647 <212> DNA <213> Bacteriophage MX9 gtggcgctca ggggtgcgtc ggacgccact accaacccct ctcgacttgt gcagtccgtc 60 geogeoggee egegtgegae teegtggggt gteagtgegt egtggtaeet getagggegt 120 acagcaacgg gggagtacat cgtgagtagc gacgcggcga agaagggcca tccaatggca 180 actgcggcgg agcggttgcc gacgtcacca atcgacgtca acgctctggc gctggaggtg 240 gcccggcttg tggccctcca gcagcaaagt gcgacgccgc catcgtccgg ccgcactttc 300 ggcgcggtgg cggatgactg gctcatcact gaggccaagc gcctcgtgtg ccccgacaat 360 qaqcqccqcc atcttcqcca tatqqaqqcq ctctqqqqca tqacqqatqt qgaqctcacq 420 ccgcgcgtcg tgaaggcgca cctggcggga cttctcaagc cagaggggcc gctgagcgca 480 gccaccgtca ataaggtgcg ctctaccggc aagcgcatca tcaaggcggc gcaaatcaac 540 qqcqaqtqqq qcccqqtqaa tcctttcqqc qtqctcqacc qcqaaaaaaqa qgcqaagqcc 600 gagcgcctca cgctgacggc agcggagtgc cgggcggtgc tcccgcactt ccgcgcggac 660 cggcqccqcq agtttctctt ccaggtcttt ctggggccac gccccggcga agagaaggcg 720 ctcctcaagg aagatgtgga cgtcgaggcg cgcaccgtca ttttccggcg cagcaatgga 780 cgagacacga caaagacggg acgcgagcgt cgcgtgccgg tgccggatga gttgtggccc 840 gtgctcctcg atgcgatgca ggccagtccg tctgacctcg ttttcccgaa cgcgaagggt 900 gagaggcagc gcgcagacac gaagatgacg cgcgtgctgc gcactgcgct atccgcggct 960 ggtgtcgtgg tgggctggga ttacatctgc cgcacgcagg gctgcggcta ccgagatgtg 1020 cagtetggtg gegegegea ggagegtegg tgeeeegeet gegacaageg catgtgggee 1080 agtggtcgcc ccaaacccgc cgtctggtac gggctccgtc acaccgcggc gacactgcac 1140 aggaaggegg gctgcgaccc gctcgtcatc aagctcgtgc tggggcatgc ggctgtcgac 1200 accacggacg acgtgtacac gcacctcgac gaggactact gccgcgccga acttaacaag 1260 ttgtcgctga aggccccgcc gccaccacct actcaccagg gaggaagtga cggcggccct 1320 qactcaggac gcaacaccta cggtgaagga ggcaccatgc acggattggg agatttgcag 1380 catcaccggg cgagagcttg ggaagctcgt gctctaccaa ctgagctacc accgcggaac 1440 ttggccgggg gtataccggc gccgctgctg agcgtcaagg acgttgcggc ttcactcta 1500 gtgagcacgg cgaaggtgta ccagctcctc gccgccggcg tcctgcctac cgtgtgggtg 1560 ggccagtcgc gccgcgtcaa gcgtgaggac ctggacgcct acatcgcccg cgcgacggcc 1620 1647 accggcggga agcggggtgg caaatga <210> 2 <211> 548 <212> PRT

<213> Bacteriophage MX9

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Arg Ala Trp Glu Ala Arg Ala Leu Pro Thr Glu Leu Pro Pro Arg Asn
                    470
                                        475
Leu Ala Gly Gly Ile Pro Ala Pro Leu Leu Ser Val Lys Asp Val Ala
                485
                                    490
Ala Ser Leu Ser Val Ser Thr Ala Lys Val Tyr Gln Leu Leu Ala Ala
            500
                                505
                                                     510
Gly Val Leu Pro Thr Val Trp Val Gly Gln Ser Arg Arg Val Lys Arg
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                                                 525
Glu Asp Leu Asp Ala Tyr Ile Ala Arq Ala Thr Ala Thr Gly Gly Lys
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                                            540
Arg Gly Gly Lys
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atgccqcctq qcttqcacat aqqqattcqa aacctcqacc ccgaqcttqq qaaqctcqtq 180
ctctaccaac tgagctacca ccgcaggcga agcagggcgc aaagtacggg ccgccctgtg 240
gcttgtcaac gggaagtgag gtgctactcc gtctcctcga cggtgagctg gtacgagtcc 300
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gccttcatgg gtgagcggcg gaagggattc gaaccctcga ccccgagctt gggaagctcg 180
tgctctacca actgagctac caccgcaggc gaagcagggc gcaaagtacg ggccgccctg 240
tggcttgtca acgggaagtg aggtgctact ccgtctcctc gacggtgagc tggtacgagt 300
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cacgcgatgc cgcctggctt gcacataggg attcgaaacc tcgaccccga gcttggqaaq 120
cteggeeteg acceptecag gegttateag cegttegeaa accettaett egeettgggg 180
attccqqqcc qqqqqcctqt ccatccqtcq caqcqqqtag caqqqqaqtct caqqqqqqtt 240
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gggaagctcg tgctctacca actgagctac caccgcggaa cttggccggg ggtataccgg 180
cgccgctgct gagcgtcaag gacgttgcgg cttcactctc agtgagcacg gcgaaggtgt 240
accagetect egeegee
                                                                    257
<210> 8
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<212> DNA
<213> Artificial Sequence
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<223> Synthetic Construct
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<212> DNA
<213> Myxococcus xanthus
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<210><211><211><212><213>	28				
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Z2105	10				

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ataattgatt ggtatgcaaa attcaagcgt ggtgaaatga gcacggagga cggtgaacgc 180
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cqtqttqqtc atatcattca tcaatatttg gatatqcgga agctctgtgc aaaatgggtg 360
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cagctqttaa ctcgtaatac acccgagttt ttccgtcgat atgtgacaat ggatgaaaca 480
tggctccatc actacactcc tgagtccaat cgacagtcgg ctgagtggac agcgaccggt 540
quaccettctc cquagectqq anaquetcan andtecqetq qcanagtant ggeetetqtt 600
tttttcqatq cqcatqqaat aatttttatc qattatcttg agaaqqqaaa aaccatcaac 660
agtgactatt atatggcgtt attggagcgt ttgaaggtcg aaatcgcggc aaaacggccc 720
catatgaaga agaaaaagt gttgttccac caagacaacg caccgtgcca caagtcattg 780
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       20
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      348
<212>
      PRT
<213> Chrysoperla carnea (Insect)
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Gly Lys Asn Thr Val Glu Ala Lys Thr Trp Leu Asp Asn Glu Asn Pro
                                2.5
Asp Ser Ala Pro Gly Lys Ser Thr Ile Ile Asp Trp Tyr Ala Lys Phe
                            40
Lys Arg Gly Glu Met Ser Thr Glu Asp Gly Glu Arg Ser Gly Arg Pro
                        55
                                            60
Lys Glu Val Val Thr Asp Glu Asn Ile Lys Lys Ile His Lys Met Ile
                    70
                                        75
Leu Asn Asp Arg Lys Met Lys Leu Ile Glu Ile Ala Glu Ala Leu Lys
                85
                                    90
Ile Ser Lys Glu Arg Val Gly His Ile Ile His Gln Tyr Leu Asp Met
                                105
Arg Lys Leu Cys Ala Lys Trp Val Pro Arg Glu Leu Thr Asn Asp Gln
                            120
                                                125
Lys Gln Gln Arg Val Asp Asp Ser Glu Arg Cys Leu Gln Leu Leu Thr
                        135
                                            140
Arg Asn Thr Pro Glu Asn Phe Arg Arg Tyr Val Thr Met Asp Glu Thr
                                        155
145
                    150
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Trp Leu His His Tyr Thr Pro Glu Ser Asn Arg Gln Ser Ala Glu Trp Thr Ala Thr Gly Glu Pro Ser Pro Lys Arg Gly Lys Thr Gln Lys Ser Ala Gly Lys Val Met Ala Ser Val Asn Phe Asp Ala His Gly Ile Ile Asn Ile Asp Tyr Leu Glu Lys Gly Lys Thr Ile Asn Ser Asp Tyr Tyr Met Ala Leu Leu Glu Arg Leu Lys Val Glu Ile Ala Ala Lys Arg Pro His Met Lys Lys Lys Val Leu Phe His Gln Asp Asn Ala Pro Cys His Lys Ser Leu Arg Thr Met Ala Lys Ile His Glu Leu Gly Phe Glu Leu Leu Pro His Pro Pro Tyr Ser Pro Asp Leu Ala Pro Ser Asp Asn Phe Leu Phe Ser Asp Leu Lys Arg Met Leu Ala Gly Lys Lys Asn Gly Cys Asn Glu Glu Val Ile Ala Glu Thr Glu Ala Tyr Asn Glu Ala Lys Pro Lys Glu Tyr Tyr Gln Asn Gly Ile Lys Lys Leu Glu Gly Arg Tyr Asn Arg Cys Ile Ala Leu Glu Gly Asn Tyr Val Glu